

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/499,468

DATE: 03/16/2001
TIME: 15:36:20

Input Set : D:\PF112U1.txt
Output Set: N:\CRF3\03162001\I499468.raw

ENTERED

50

98

146

194

242

290

RECEIVED
MAR 23 2001
TECH CENTER 1600/2900

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69	55	60	65	70	
71	aga gaa cag gcc aac	ctc aac tca agg	aca gaa gag act ata	aaa ttt	338
72	Arg Glu Gln Ala Asn	Leu Asn Ser Arg Thr	Glu Glu Thr Ile Lys	Phe	
73		75	80	85	
75	gct gca gca cat tat	aat aca gag atc ttg	aaa agt att gat aat	gag	386
76	Ala Ala Ala His Tyr	Asn Thr Glu Ile Leu	Lys Ser Ile Asp Asn	Glu	
77		90	95	100	
79	tgg aga aag act caa	tgc atg cca cgg gag	gtg tgt ata gat gtg	ggg	434
80	Trp Arg Lys Thr Gln	Cys Met Pro Arg Glu	Val Cys Ile Asp Val	Gly	
81		105	110	115	
83	aag gag ttt gga gtc	gcg aca aac acc ttc	ttt aaa cct cca tgt	gtg	482
84	Lys Glu Phe Gly Val	Ala Thr Asn Thr Phe	Phe Lys Pro Pro Cys	Val	
85		120	125	130	
87	tcc gtc tac aga tgt	ggg ggt tgc tgc aat	agt gag ggg ctg cag	tgc	530
88	Ser Val Tyr Arg Cys	Gly Gly Cys Cys Asn	Ser Glu Gly Leu Gln	Cys	
89	135	140	145	150	
91	atg aac acc agc acg	agc tac ctc agc aag	acg tta ttt gaa att	aca	578
92	Met Asn Thr Ser Thr	Ser Tyr Leu Ser Lys	Thr Leu Phe Glu Ile	Thr	
93		155	160	165	
95	gtg cct ctc tct caa	ggc ccc aaa cca gta	aca atc agt ttt gcc	aat	626
96	Val Pro Leu Ser Gln	Gly Pro Lys Pro Val	Thr Ile Ser Phe Ala	Asn	
97		170	175	180	
99	cac act tcc tgc cga	tgc atg tct aaa ctg	gat gtt tac aga caa	gtt	674
100	His Thr Ser Cys Arg	Cys Met Ser Lys Leu	Asp Val Tyr Arg Gln	Val	
101		185	190	195	
103	cat tcc att att aga	cgt tcc ctg cca gca	aca cta cca cag tgt	cag	722
104	His Ser Ile Ile Arg	Arg Ser Leu Pro Ala	Thr Leu Pro Gln Cys	Gln	
105		200	205	210	
107	gca gcg aac aag acc	tgc ccc acc aat tac	atg tgg aat aat cac	atc	770
108	Ala Ala Asn Lys Thr	Cys Pro Thr Asn Tyr	Met Trp Asn Asn His	Ile	
109	215	220	225	230	
111	tgc aga tgc ctg gct	cag gaa gat ttt atg	ttt tcc tcg gat gct	gga	818
112	Cys Arg Cys Leu Ala	Gln Glu Asp Phe Met	Phe Ser Ser Asp Ala	Gly	
113		235	240	245	
115	gat gac tca aca gat	gga ttc cat gac atc	tgt gga cca aac aag	gag	866
116	Asp Asp Ser Thr Asp	Gly Phe His Asp Ile	Cys Gly Pro Asn Lys	Glu	
117		250	255	260	
119	ctg gat gaa gag acc	tgt cag tgt gtc tgc	aga gcg ggg ctt cgg	cct	914
120	Leu Asp Glu Glu Thr	Cys Gln Cys Val Cys	Arg Ala Gly Leu Arg	Pro	
121		265	270	275	
123	gcc agc tgt gga ccc	cac aaa gaa cta gac	aga aac tca tgc cag	tgt	962
124	Ala Ser Cys Gly Pro	His Lys Glu Leu Asp	Arg Asn Ser Cys Gln	Cys	
125		280	285	290	
127	gtc tgt aaa aac aaa	ctc ttc ccc agc caa	tgt ggg gcc aac cga	gaa	1010
128	Val Cys Lys Asn Lys	Leu Phe Pro Ser Gln	Cys Gly Ala Asn Arg	Glu	
129	295	300	305	310	
131	ttt gat gaa aac aca	tgc cag tgt gta tgt	aaa aga acc tgc ccc	aga	1058
132	Phe Asp Glu Asn Thr	Cys Gln Cys Val Cys	Lys Arg Thr Cys Pro	Arg	
133		315	320	325	

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135 aat caa ccc cta aat cct gga aaa tgt gcc tgt gaa tgt aca gaa agt      1106
136 Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser
137          330          335          340
139 cca cag aaa tgc ttg tta aaa gga aag aag ttc cac cac caa aca tgc      1154
140 Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys
141          345          350          355
143 agc tgt tac aga cgg cca tgt acg aac cgc cag aag gct tgt gag cca      1202
144 Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro
145          360          365          370
147 gga ttt tca tat agt gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg      1250
148 Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp
149 375          380          385          390
151 caa aga cca caa atg agc taagattgta ctgttttcca gttcatcgat      1298
152 Gln Arg Pro Gln Met Ser
153          395
155 tttctattat ggaaaactgt gttgccacag tagaactgtc tgtgaacaga gagacccttg      1358
157 tgggtccatg ctaacaaaga caaaagtctg tctttcctga accatgtgga taactttaca      1418
159 gaaatggact ggagctcatc tgcaaaaggc ctcttgtaaa gactggtttt ctgccaatga      1478
161 ccaaacagcc aagattttcc tcttgtgatt tctttaaaag aatgactata taatttattt      1538
163 ccaactaaaaa tattgtttct gcattcatit ttatagcaac aacaattggg aaaactcact      1598
165 gtgatcaata tttttatatt atgcaaaaata tgtttaaaat aaaatgaaaa ttgtatttat      1658
167 aaaaaaaaaa aaaaaa      1674
170 <210> SEQ ID NO: 2
171 <211> LENGTH: 419
172 <212> TYPE: PRT
173 <213> ORGANISM: homo sapiens
175 <400> SEQUENCE: 2
177 Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
178          -20          -15          -10
181 Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe
182          -5          -1 1          5
185 Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
186 10          15          20          25
189 Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
190          30          35          40
193 Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
194          45          50          55
197 Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
198          60          65          70
201 Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
202          75          80          85
205 His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
206 90          95          100          105
209 Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
210          110          115          120
213 Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
214          125          130          135
217 Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
218          140          145          150

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221 Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
222      155      160      165
225 Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
226 170      175      180      185
229 Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
230      190      195      200
233 Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
234      205      210      215
237 Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
238      220      225      230
241 Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
242      235      240      245
245 Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
246 250      255      260      265
249 Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
250      270      275      280
253 Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
254      285      290      295
257 Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
258      300      305      310
261 Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
262      315      320      325
265 Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
266 330      335      340      345
269 Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
270      350      355      360
273 Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
274      365      370      375
277 Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro
278      380      385      390
281 Gln Met Ser
282      395
285 <210> SEQ ID NO: 3
286 <211> LENGTH: 1526
287 <212> TYPE: DNA
288 <213> ORGANISM: homo sapiens
290 <400> SEQUENCE: 3
291 cgaggccacg gcttatgcaa gcaaagatct ggaggagcag ttacggtctg tgtccagtgt      60
293 agatgaactc atgactgtac tctaccaga atattgaaa atgtacaagt gtcagctaag      120
295 gaaaggaggc tggcaacata acagagaaca ggccaacctc aactcaagga cagaagagac      180
297 tataaaattt gctgcagcac attataatac agagatcttg aaaagtattg ataatgagtg      240
299 gagaaagact caatgcatgc cacgggaggt gtgtatagat gtggggaagg agtttgaggt      300
301 cgcgacaaac accttcttta aacctccatg tgtgtccgtc tacagatgtg ggggttgctg      360
303 caatagttag gggctgcagt gcatgaacac cagcacgagc tacctcagca agacgttatt      420
305 tgaaattaca gtgcctctct ctcaaggccc caaaccagta acaatcagtt ttgccaatca      480
307 cacttctctc cgatgcatgt ctaaactgga tgtttacaga caagttcatt ccattattag      540
309 acgttccctg ccagcaacac taccacagtg tcaggcagcg aacaagacct gccccaccaa      600
311 ttacatgttg aataatcaca tctgcagatg cctggctcag gaagatttta tgttttctc      660
313 ggatgctgga gatgaactca cagatggatt ccatgacatc tgtggacca acaaggagct      720

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315 ggatgaagag acctgtcagt gtgtctgcag agcggggcctt cggcctgcc a gctgtggacc 780
317 ccacaaagaa ctagacagaa actcatgcc a gtgtgtctgt aaaaacaaac tcttccccag 840
319 ccaatgtggg gccaacgcag aatttgatga aaacacatgc cagtgtgtat gtaaaagaac 900
321 ctgccccaga aatcaacccc taaatcctgg aaaatgtgcc tgtgaatgta cagaaagtcc 960
323 acagaaatgc ttgttaaaag gaaagaagtt ccaccaccaa acatgcagct gttacagacg 1020
325 gccatgtacg aaccgccaga aggcttctga gccaggattt tcatatagtg aagaagtgtg 1080
327 tcgttgtgtc ccttcatatt ggcaaagacc acaaatgagc taagattgta ctgttttcca 1140
329 gttcatcgat tttctattat ggaaaactgt gttgccacag tagaactgtc tgtgaacaga 1200
331 gagacccttg tgggtccatg ctaacaaaga caaaagtctg tctttcctga accatgtgga 1260
333 taactttaca gaaatggact ggagctcatc tgcaaaaggc ctcttgtaaa gactgggttt 1320
335 ctgccaatga ccaaacagcc aagattttcc tcttctgatt tctttaaaag aatgactata 1380
337 taattttatt ccaactaaaa tattgtttct gcattcatct ttatagcaac aacaattggt 1440
339 aaaactcact gtgatcaata tttttatatt atgcaaaata tgtttaaaat aaaatgaaaa 1500
341 ttgtatttat aaaaaaaaaa aaaaaa 1526
344 <210> SEQ ID NO: 4
345 <211> LENGTH: 350
346 <212> TYPE: PRT
347 <213> ORGANISM: homo sapiens
349 <400> SEQUENCE: 4
351 Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu
352 1 5 10 15
354 Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn Leu Asn Ser
355 20 25 30
357 Arg Thr Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu
358 35 40 45
360 Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro
361 50 55 60
363 Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn
364 65 70 75 80
366 Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys
367 85 90 95
369 Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr Leu
370 100 105 110
372 Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys
373 115 120 125
375 Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser
376 130 135 140
378 Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu
379 145 150 155 160
381 Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro Thr
382 165 170 175
384 Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala Gln Glu Asp
385 180 185 190
387 Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp Gly Phe His
388 195 200 205
390 Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys
391 210 215 220
393 Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro His Lys Glu
394 225 230 235 240

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fyI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8